

The theoretical study of anticancer rhodium complexes and methyl groups effect on ligands in chemical reactivity, global descriptors, ADMET by DFT study

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Abstract:

As there are a potential application of rhodium (0) complexes and rhodium (II) complexes in anticancer drug discovery, the key point of this study is to design new rhodium(0) complexes with amine ligand, and was estimated their properties. To predict the thermo-physical, chemical reactivity and biological activity of most expected rhodium (0) complexes with amine and alkyl amine were conducted by the computational method of density functional theory (DFT). The thermo-physical parameters, such as free energy, entropy, dipole moment, binding energy, nuclear energy, electronics energy and heat of formation were calculated, as well as chemical reactivity, for example, Highest Occupied Molecular Orbital (HOMO), Lowest Unoccupied Molecular Orbital (LUMO) and HOMO-LUMO gap. Some descriptors, such as ionization potential, electronegativity, hardness, softness and electron affinity were estimated of rhodium (0) complexes. To explain about biological indication, the charge density, surface area grid, volume, LogP, polarizability, refractivity and molecular mass had also calculated. The ADMET was illustrated through the online database AdmetSAR for the safe uses and toxicological evidence. Regarding the chemical reactivity study in view of softness and LUMO HOMO gap, the L03 is a more suitable drug than others, and stands for that secondary alkyl amine as ligand is more effective than primary and tertiary amine ligands.

Keywords: Rhodium, QSAR, HOMO, LUMO, IR and ADMET.

1. Introduction

Presently, Cancer has known as the world's largest killer disease, and more than 100 types of cancer have been identified by the scientists, most of which are found as breast cancer, skin cancer, lung cancer, colon cancer, prostate cancer and lymphoma cancer [1-3]. No medical system and treatment could fully discover its proper remedy and drugs. For some of the cancers, there are given chemotherapy or radiotherapy, but it can be partially treated for temporary fit from the disease [4, 5]. Nevertheless, hope is that at the present time, scientists are doing the greatest work in cancer research and research. The most active compound in anti-cancer drugs had used still the complex

compound of transition metals. The most used metal for making complex is palladium, rhodium, cadmium, bismuth and silver nanotechnology particle [6]. Along with the complex compounds of transition metals, some of the ionic liquids, natural products, and heterocyclic compounds are being used [7, 8].

Experimental work in chemistry, as well as in the present day, computational chemistry is going to the same level by which a chemist can easily design an anticancer drug. For theoretical studies, a future-based data onto various types of physical, chemical, and biological activity to those elements can be made. The computational chemistry's role is important for these theoretical studies, because of

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which there is a conception of a molecule without any chemical substance and all simulations can be done for future studies of their property. For this reason, some of the rhodium complexes about anticancer molecules are designed to use as an anticancer drug. By using the Density functional theory (DFT), the designated molecular physical properties, such as entropy, heat capacities, binding energy and electronic energy, are determined [9-11]. Using quantum mechanics, the Frontier molecular orbital has been derived, and the HOMO and LUMO, and chemical reactivity can be found and the HOMO, LUMO and HOMO-LUMO gap trends to explain the chemical reactivity of organic molecules, the larger energy gap indicate the less stability and higher tendency for dissociation as bioactive molecules [12-24].

What are the main points of our study that we have used QSAR data and ADME data to determine their biological activity? The important data onto QSAR studies is a LogP that allows measuring the toxicity level of a compound. In our work, we have used this data to determine the hydrophobicity and the hydrophobicity.

In this study, rhodium complexes optimized with DFT/B3LYP [25]. Some geometrical parameters and HOMO-LUMO energy level of the complex were calculated at B3LYP. Their molecular structural relationship, HOMO, LUMO, and quantum chemical properties and LogP plays the role of the chemical reactivity, biological activity and hydrophobicity and hydrophobicity of chemicals in relation with living cells activity and associated mechanistic interactions [8, 12, 13, 26]

2. Computational Method

2.1. Determination of thermophysical

The molecular modelling program permits to build and analyze different molecular structures and determine the thermophysical properties, QSAR using HyperChem 8.010 version. In order to create the spatial chemical structure of each calculated molecule, the two-dimensional structure of the molecule shall be built step-by-step by drawing. Then hydrogen atoms are automatically added from building option and chemical structure is converted into a 3D structure. The first step in getting the main characteristic parameters of molecules is to optimize the molecular structure to obtain a configuration characterized by minimum free

energy. In sitting, the DFT was fixed via 321G*, and B3-LYP [27]. After completing optimization, the free energy, entropy, dipole moment, binding energy, nuclear energy, electronics energy, the heat of formation, QSAR and electrostatic potential were recorded.

2.2. Optimization of chemical reactivity (HOMO LUMO), and electrostatic potential and IR

All molecules were optimized by Gaussian 16 professional [28, 29] for molecular geometry. After optimization, the B3LYP functional of DFT method was used for calculating chemical reactivity and IR frequency. This optimized structures were visualized in material studio version 8 [30] for taking the diagram of HOMO-LUMO and 3D map of electrostatics potential.

2.3. Determination the data of ADMET

The Input/output system consists of input or output of the strings, commands and files. ADMET lab uses the functions like file, open, write, get current working directory (getcwd) and set current working directory (setcwd) from Python I/O system to accomplish the file reads and writes. For calculating absorption, distribution, metabolism, excretion and toxicity "ADMET Prediction," there are two options of files types such as SMILES and SDF. The three input ways are inputting SMILES, uploading files and drawing molecules. After inputs files, it was loaded and needed a few minutes for calculation at all point which was obtained as the outputs data table. CSV file even these stored files were downloaded as HTML page which contains interactive data table of all satisfied items. This job was completed in following link <http://lmmd.ecust.edu.cn/admet2> [31-34].

3. Results and discussion

3.1. Optimized structure

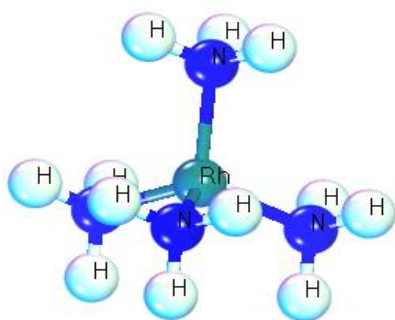
The optimized structure represents the molecular symmetry. In figure-01, four rhodium (0) complexes named as Tetraaminorhodium (L01), Tetraamino (N-methyl) rhodium (L02), Tetraamino (N, N-dimethyl) rhodium(L03) and Tetraamino (N, N, N-trimethyl)rhodium (L04) having both of molecular symmetry and asymmetry properties.

3.2. HOMO-LUMO

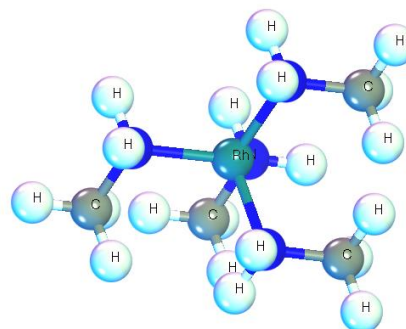
The HOMO and LUMO for different Rhodium (0) complexes gives about the possible electronic transition from lower energy level to higher energy level and indicate the electrophilic and nucleophilic attraction region in the molecule. The LUMO-HOMO gap is recognized as the most vital parameter for chemical reactivity. The shorter LUMO- HOMO gap is considered as the high

reactivity as well as more biologically active molecules, they are highlighted in figure 2 and table-01 (colour: green is a positive value and blue is a negative value). The HOMO can be through the outermost orbital containing electrons tends to give these electrons such as an electron donor besides LUMO can be through the innermost orbital containing free places to accept an electron.

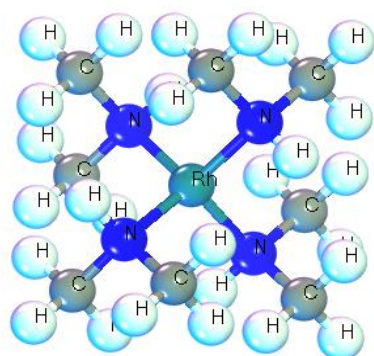
Tetraaminorhodium, (L01)



Tetraamino (N-methyl) rhodium, (L02)



Tetraamino (N,N-dimethyl) rhodium, (L03)



Tetraamino (N,N,N-trimethyl) rhodium , (L04)

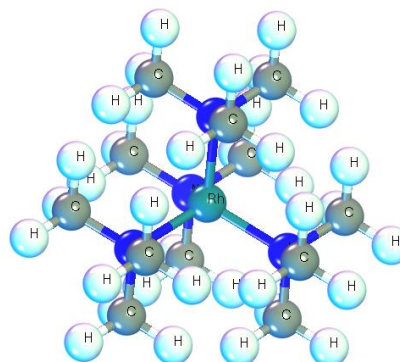


Figure 1. Optimized structure in the cylinder shape.

3.3. Chemical reactivity by DFT Calculations

The chemical reactivity of drug and its aptitude to bind with a given protein are basically determined by frontier orbitals' energy value. HOMO along can be a vital factor to find the relationship between a class of drug's action and their electronic configuration [35]. A recent report reveals that in protein-drug interaction only exists on LUMO of protein and HOMO of its drug.

The Energy of the HOMO is directly related to the ionization potential, and LUMO Energy is directly related to the electron affinity. The energy

difference between HOMO and LUMO orbital is called an energy gap which is an important parameter that determines the stability of the structures. The energy gap is used in molecular electrical transport properties [11]. In addition, according to Koopmans' theorem the energy gap, E_{gap} , defined as the difference between HOMO and LUMO energy [36].

$$E_{\text{gap}} = (E_{\text{LUMO}} - E_{\text{HOMO}}) \approx \text{IP} - \text{EA}$$

The ionization potential (I) and electron affinity (A) can be estimated from the HOMO and

LUMO energy values as the following equation and given in table -01.

$$I = -E_{HOMO} \quad (1)$$

$$A = -E_{LUMO} \quad (2)$$

The HOMO and LUMO energies are used for the determination of global descriptors, such as electrophilicity (ω), a chemical potential (μ), electronegativity (χ), hardness (η) and softness (S), and the output data was recorded in table-01. We focus on the HOMO and LUMO energies in

order to determine the global descriptors by following equations [37-39]

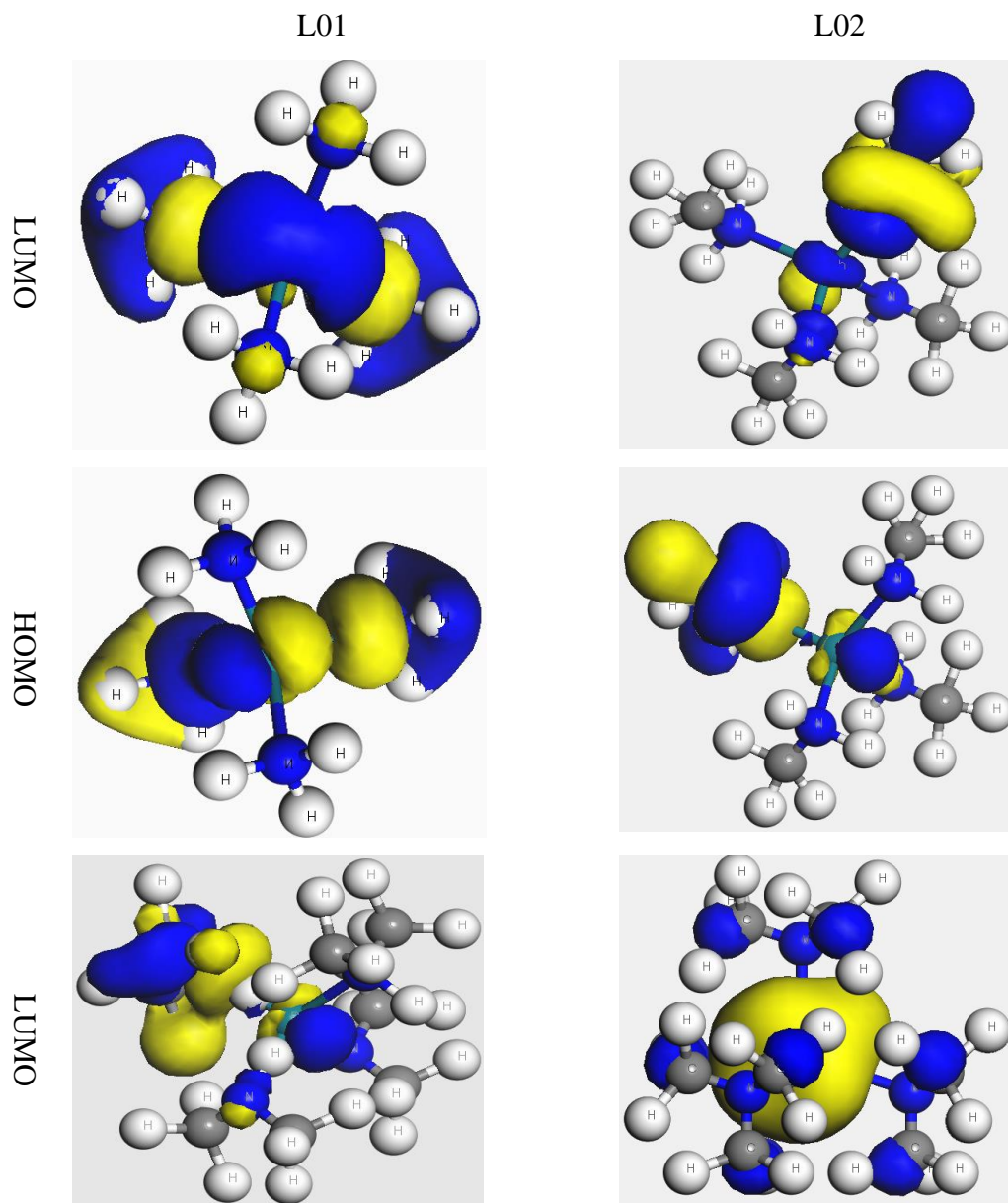
$$(\mu) = -\frac{I+A}{2} \quad (3)$$

$$(\eta) = \frac{I-A}{2} \quad (4)$$

$$(S) = \frac{1}{\eta} \quad (5)$$

$$(\chi) = \frac{I+A}{2} \quad (6)$$

$$(\omega) = \frac{\mu^2}{2\eta} \quad (7)$$



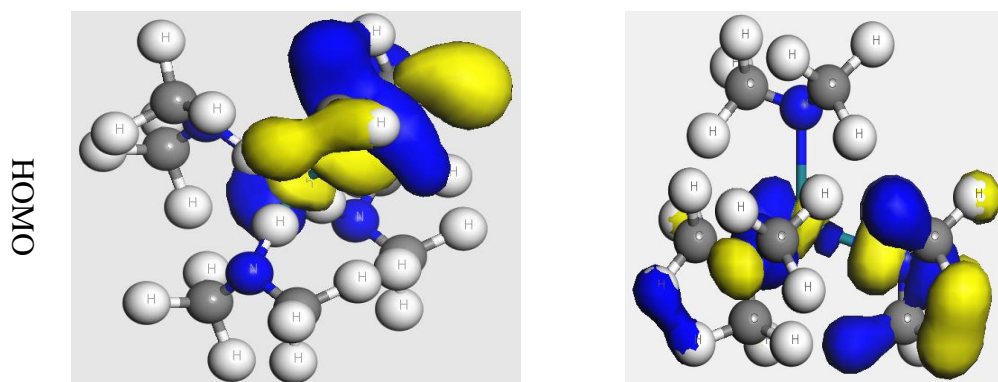


Figure 2. HOMO LUMO frontier molecular orbital diagram

Table 1. Data for chemical reactivity and Global descriptors

	L01	L02	L03	L04
LUMO (0), eV	-2.886	-1.158	-0.590	-1.274
HOMO (0), eV	-7.534	-6.035	-5.979	-6.070
ΔE , (LUMO-HOMO)	4.648	4.877	5.389	4.796
Ionization potential (I), eV	7.534	6.035	5.979	6.070
Electron affinity (A), eV	2.886	1.158	0.590	1.274
Hardness, (η)	2.324	2.438	2.694	2.398
Softness, (S)	0.430	0.410	0.371	0.417
Electrophilicity (ω),	6.075	1.641	2.001	2.811
Chemical potential, (μ)	-5.210	-3.596	-3.284	-3.672
Electronegativity, (χ)	5.210	3.596	3.284	3.672

3.4. Thermophysical properties

The binding free energy of the optimized molecules is calculated by performing docking process. The molecule with minimum binding energy will have the maximum binding affinity and indicates as the best molecule for drug lead molecules targeting computationally. We can find out the drug binding affinity by using the fitness of the drug, which can bind to the target molecule during the docking process, and the second way is using Gibbs free energy calculations. According to this more negative value, we can consider a more effective drug.

The bond dipole moment is the idea of an electric dipole moment to measure the polarity of a

chemical bond between a molecule. In view of pharmaceutical industries, the dipole moment was a parameter for the drug by which a drug is to be used open or close packet. If any drug has a dipole moment, it can be able to absorb the ultraviolet light and have a possibility of properties. The four optimized ILs show zero dipole moment so that it can be used without any protection against UV or sunlight. The total energy, free energy, dipole moment, binding energy, Heat of formation and nuclear energy are given in table-02. The entropy and heat capacity is changed into changing temperature. The activity of temperature is listed in table 03.

Table 2. Thermophysical properties

Properties	L01	L02	L03	L04
Total energy, (kcal/mol)	-46786.401	-65992.512	-86694.847	-106501.928
Free energy, (kcal/mol)	-46786.401	-65992.512	-86694.847	-106501.928
RMS gradient, (kcal/mol)	0.815	0.001	0.065	0.001
Binding energy, (kcal/mol)	-2921.649	-5586.162	-9746.900	-13012.384
Heat of formation, (kcal/mol)	-1711.425	-3275.563	-6335.924	-8501.032
Electronic energy, (kcal/mol)	-158326.626	-326716.780	-518479.774	-761863.712
Nuclear energy, (kcal/mol)	111540.225	260724.268	431784.927	655361.784

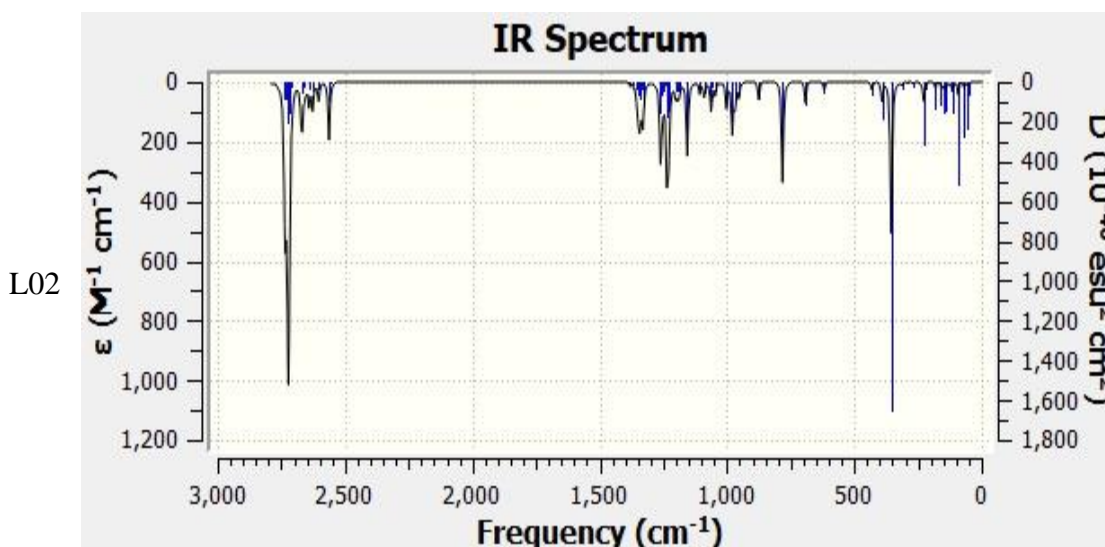
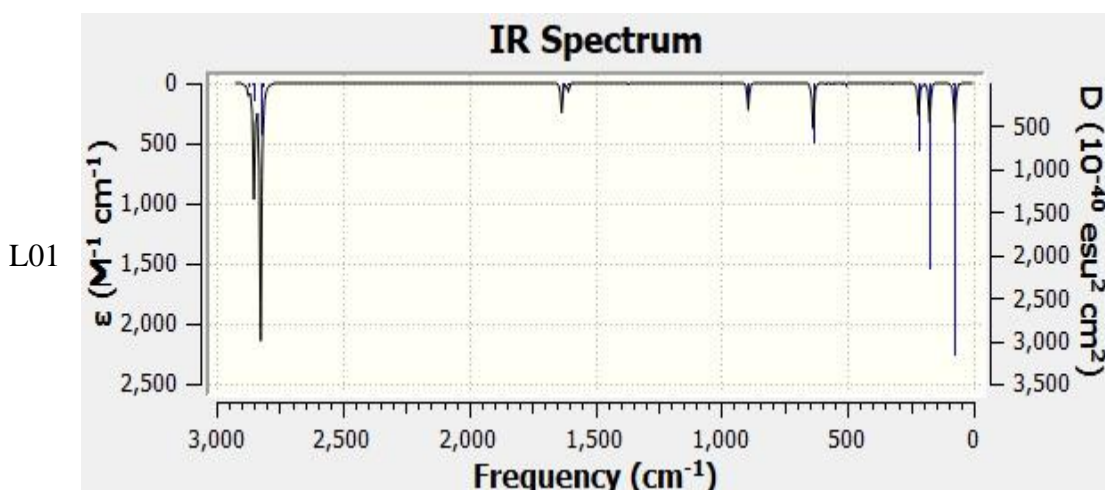
Table 3. Entropy and Heat capacity in different temperature

	273 K		298 K		323 K	
	Entropy	Heat capacity, (kcal/mol-deg)	Entropy	Heat capacity, (kcal/mol-deg)	Entropy	Heat capacity, (kcal/mol-deg)
L01	0.0788	0.0285	0.0816	0.0307	0.0843	0.0328
L02	0.0933	0.0430	0.0974	0.0468	0.1015	0.050
L03	0.1051	0.0519	0.1100	0.0561	0.1148	0.0602
L04	0.1196	0.0563	0.1248	0.0598	0.1300	0.0636

3.5. Computing the IR spectrum for characterization

The IR spectrum was calculated by optimization and frequency calculation using Gaussian software 16W packet which indicated the characteristic peak for identification of various functional groups. In the rhodium (0) tetraamino compounds were made by some groups, such as CH₃ and NH₃ where the C-C, C-H, C-N, and N-H stretching could be found.

For L01, there are two peak at about 2850 and 2800 cm⁻¹ for N-H stretching, 1650 to 1580 cm⁻¹ for N-H bending peak and 910- 666 cm⁻¹ peak for N-H vibration. In general, the methyl groups have attached with L02, L03 and L04 in which the C-H, -N-CH₃ or -N-C-H peak are found. Here, it has to be noted that 2805 -2780 cm⁻¹ peak is for -N-CH₃ and 2800 -2900 for C-H stretching. The IR peak of optimized molecules represents in figure no 03.



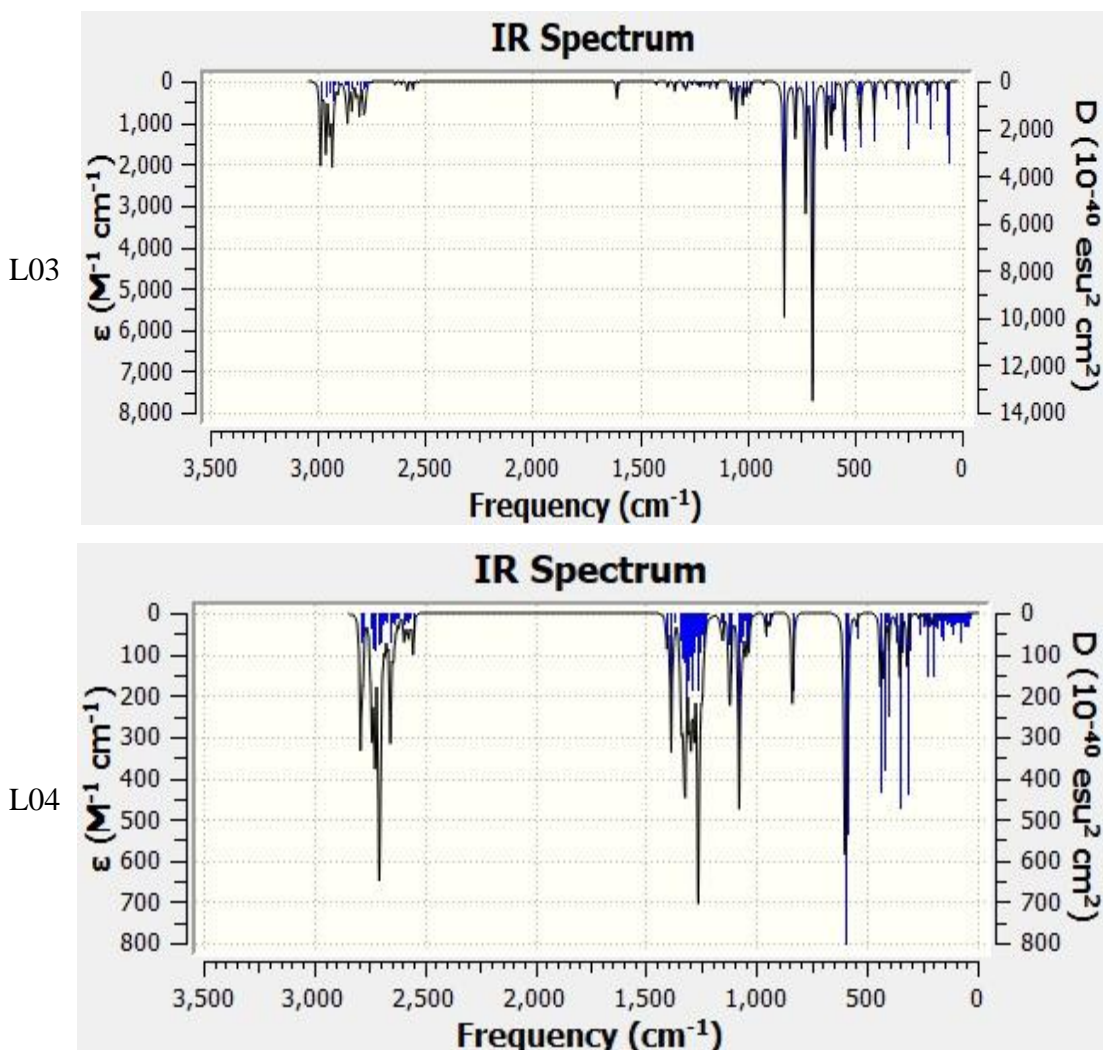


Figure 3. Computing IR spectrum from Gaussian

3.6. QSAR study

The stability of the studied molecules is also conducted by electrostatic potential charges distribution, and QSAR data predicts their correlation on the basis of structure. The QSAR data represents in table 4. From table 4, it is found that the value of LogP for all four molecules is negative and stands for hydrophilic nature. With the

increasing number of attaching the methyl groups of the ligand, the value is gradually decreased. As a result, it could be said that hydrophobicity decreases. Conversely, hydrophilic drugs which have low octanol/water partition coefficients are found primarily in aqueous regions such as blood serum.

Table 4. Data for QSAR study

	L01	L02	L03	L04
Surface Area(grid), Å ²	258.86	324.79	394.26	430.39
Volume, Å ³	352.25	505.68	670.35	775.14
Hydration Energy ,kcal/mol	-43.29	-8.56	1.26	4.68
Log P	-3.91	-2.93	-1.94	-1.95
Refractivity, Å ³	9.60	29.19	48.77	68.36
Polarizability, Å ³	4.68	12.02	19.36	26.70
Mass (amu)	171.03	227.14	283.24	339.35

3.7. 3D mapped structure in term of electrostatic potential map

The electrostatic potential charge distribution 3D map is one of the vital key from computational tools to explain the nature of molecule as entering and binding ability in the protein of micropathogens, and larger charge distribution indicates the higher probability as drugs. The figure

4 illustrates the electrostatic potential charge distribution 3D map showing the both of positive and negative charge distribution through the full surface of molecules while red color region indicates the positive parts and yellow color mentions the negative charge. From the figure 4, it could be found that there are higher portion the positive charge in full surface of tested complexes.

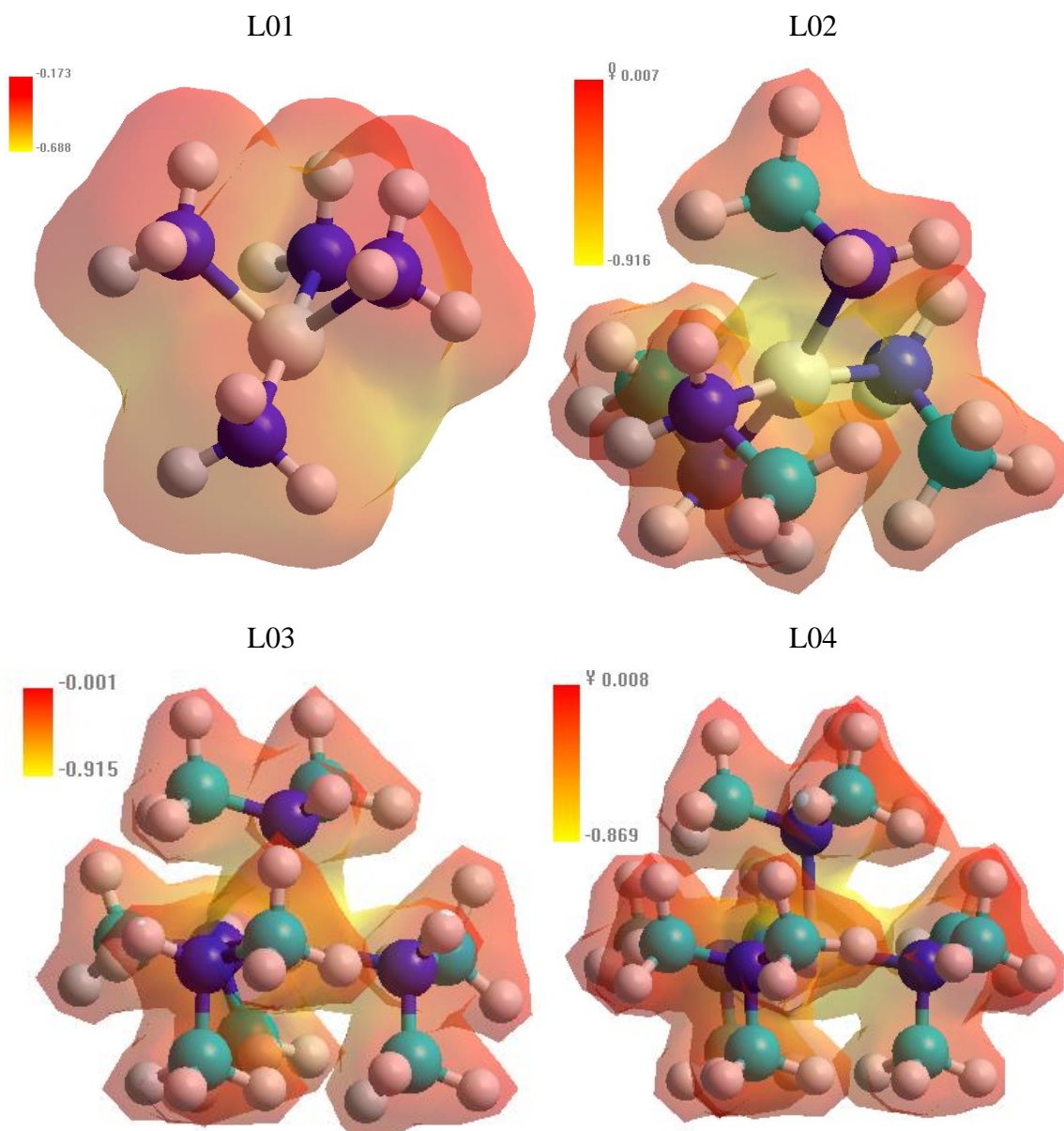


Figure 4. The 3D geometry of the electrostatic distribution potential

Here, E1=Electrostatic potential energy in positive value, E2= Electrostatic potential energy in

negative value and ΔE =Electrostatic potential energy difference of two level.

3.8. Biological Studies by ADMET

ADME stands for absorption, distribution, metabolism and excretion and ADMET is expressed the shortage form of absorption, distribution, metabolism, excretion and toxicity which are considered as the vital parts of any drug development program, and essential for compliance with regulatory guidelines. Both of these conducted for chemical optimization, process development, and pharmacological profile [40]. This study belongs to invariably involve whole-animal models which is highly time-consuming and expensive

fact. In order to minimize the cost and time, the computational data of ADME study helps to design a new drug for drug preparation or without the clinical trial. Such events created a serious disruption of the development process and often resulted in the closure of the project and a lost opportunity, as a result the situation of drug discovery has been changing rapidly and dramatically in recent time. The different data onto ADMET is listed in table 5.

Table 5. Absorption, Distribution, Metabolism, Excretion and Toxicity property of properties of rhodium (0) complexes

Property	Model Name and Unit (numeric or categorical)	Predicted Value			
		L01	L02	L03	L04
Absorption	Water solubility (log mol/L)	4.49e-3	3.72e-1	1.11e-2	4.49e-3
	CaCo2 permeability (logPapp in 10 ⁻⁶ cm/s)	0.6304	0.6310	0.7651	1.3313
	Intestinal absorption human (%)	0.8984	0.8128	0.8510	0.6175
	Skin Permeability (log Kp)	-7.62	-8.31	-7.32	-7.62
	P-glycoprotein substrate (Yes/No)	No	No	No	No
	P-glycoprotein I inhibitor (Yes/No)	No	No	No	No
	P-glycoprotein II inhibitor (Yes/No)	No	No	No	No
Distribution	Blood-Brain Barrier	No	No	No	No
	Plasma protein binding	No	No	No	No
	Estrogen receptor binding	No	No	No	No
	Androgen receptor binding	No	No	No	No
	Subcellular localization	No	No	No	No
	Glucocorticoid receptor binding	No	No	No	No
	Aromatase binding	No	No	No	No
Metabolism	Thyroid receptor binding	No	No	No	No
	CYP2D6 substrate (Yes/No)	No	No	No	No
	CYP3A4 substrate (Yes/No)	No	No	No	No
	CYP1A2 inhibitor (Yes/No)	No	No	No	No
	CYP2C19 inhibitor (Yes/No)	No	No	No	No
	CYP2C9 inhibitor (Yes/No)	No	No	No	No
	CYP2D6 inhibitor (Yes/No)	No	No	No	No
	CYP3A4 inhibitor (Yes/No)	No	No	No	No
Excretion	BSEP inhibitor (Yes/No)	No	No	No	No
	OCT2 inhibitor (Yes/No)	No	No	No	No
Toxicity	AMES toxicity (Yes/No)	No	No	No	No
	Human Ether-a-go-go-related gene Inhibition (Yes/No)	Weak	Weak	Weak	Weak
	Carcinogens (Yes/No)	No	No	No	Yes
	Honey Bee Toxicity	High	High	Low	High
	<i>T. Pyriformis</i> toxicity (Yes/No)	High	Low	Low	Low
	Biodegradation (Yes/No)	No	No	No	No
	Fish Toxicity	High	Low	High	Low
	Acute Oral Toxicity	III	III	III	III
	Oral Rat Acute Toxicity (LD50) (mol/kg)	2.3622	2.6122	2.300	2.412

<i>T. Pyriformis</i> toxicity (log ug/L)	-0.3333	-0.6998	-0.590	-0.548
Fish Toxicity pLC50 mg/L	1.8123	1.8747	1.4104	1.4973

In term of absorption, it consists of various parameters, such as water solubility, CaCo2 permeability, intestinal absorption human, skin permeability and P-glycoprotein substrate or inhibitor. From the table 5, it has found that L01, L02, L03 and L04 can show water solubility where the L01 and L04 show the lower value with close to each other. Secondly, the intestinal absorption human indicates the transporting ability in target body which is expressed in table 5 as mole fraction or fraction of one integer. L01, L02 and L03 show the value in 0.84 to 0.89 while L04 has in 0.61. On the other side, the activity of P-glycoprotein substrate or inhibitor is going to the box, negative. The rationale of the blood–brain barrier has to reveal that it protects against circulating toxins or pathogens which are responsible for brain infections, and it has been considered as the distribution. The distribution is also constituted by plasma protein binding, estrogen receptor binding, androgen receptor binding, subcellular localization, glucocorticoid receptor binding and aromatase binding, but there are no response to these parameters.

Finally, in case of excretion and toxicity, they have no response to Excretion properties and the human toxicity is week as well as non carcenognric. They can show slightly toxic against bee or fish.

4. Conclusion

In this study reports a theoretical investigation and development of rhodium (0) complexes with amine ligands for their biological significance. To design the new molecules, amine ligand was chosen, and methyl groups have been attached in terminal to evaluate their activity on thermophysical properties, chemical reactivity, global descriptors, and biological studied throughout ADMET and QSAR. The softness of two methyl containing ligand (L03) shows the lowest among others, meaning highly biological active than others while hardness represents inverse to softness. For identification of functional groups, IR peak was evaluated, which shows the primary, secondary and tertiary amine of the ligand. The thermophysical properties were changed as similar into chemical reactivity, whereas the two methyl groups containing ligand conducted the higher

thermophysical activity. The logP of QSAR value predicted the distribution of aqueous regions such as blood serum even though L03 is the highest distribution. Finally, the ADMET data represents some essential parameters such as these molecules are good solubility in water, non-carcinogenic and low toxic.

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